EP 0301670 (1)
C12N15/31-C12N15/62A-C12N15/59-
C12N15/58-C12N15/14-C12N15/62-

-6- BASIC DOC.- C12N15/14 (11) Publication number: 0 301 670 A1

Office européen des brevets

(12) EUROPEAN PATENT APPLICATION

(21) Application number: 88201632.2

(22) Date of filing: 28.07.88

(51) Int. Cl.⁴: C12N 15/00 , C12P 21/00 , C12N 1/16 , C12N 5/00 , C07H 21/04

The microorganism(s) has (have) been deposited with Centraal Bureau voor Schimmelcultures under number(s) CBS 184.87, CBS 872.87 and American Type Cultures Collection under numbers ATCC 20855, ATCC 20854, ATCC 67454, ATCC 67455.

The applicant has filed a statement in accordance with Rule 28 (4) EPC (issue of a sample only to an expert). Accession number(s) of the deposit(s): CBS 184.87, CBS 872.87, ATCC No. 20855, ATCC No. 20854, ATCC No. 67454, ATCC 67455.

A request for correction of figure 7 has been filed pursuant to Rule 88 EPC. A decision on the request will be taken during the proceedings before the Examining Division (Guidelines for Examination in the EPO, A-V, 2.2).

(30) Priority: 28.07.87 US 78539

(43) Date of publication of application:
01.02.89 Bulletin 89/05

(84) Designated Contracting States:
AT BE CH DE ES FR GB GR IT LI LU NL SE

(71) Applicant: GIST-BROCADES N.V.
Wateringseweg 1
NL-2611 XT Delft(NL)

(72) Inventor: van den Berg, Johannes A., Dr.
Hanegevecht 8
NL-2811 AD Reeuwijk(NL)
Inventor: van Ooyen, Albert J.J., Dr.
Laan van Heldenburg 23
NL-2271 AR Voorburg(NL)
Inventor: Rietveld, Krijn, Dr.
van der Waalsstraat 129
NL-3132 TL Vlaardingen(NL)

(74) Representative: Huygens, Arthur Victor, Dr. et al
c/o Gist-Brocades N.V. Patent & Trademarks Department Wateringseweg 1 PO Box 1
NL-2600 MA Delft(NL)

(54) Kluyveromyces as a host strain.

(57) Kluyveromyces hosts and DNA expression cassettes for use in Kluyveromyces are provided for transcription of endogenous and/or exogenous DNA, and production of peptides, for enhancing production of an endogenous product, or producing an exogenous product. The Kluyveromyces hosts find particular use for secretion of a desired peptide product, where signal sequences may be native to the peptide or provided from endogenous or exogenous signal sequences, including synthetic sequences, functional in Kluyveromyces. A transformation procedure is provided for efficiently transforming Kluyveromyces.

EP 0 301 670 A1

gene, optionally containing a signal sequence for secretion, under the transcriptional and translational regulation of the regulatory regions. The cassettes are introduced into the Kluyveromyces host strain under conditions whereby the resulting transformants stably maintain the expression cassettes. Naturally occurring DNA and synthetic genes may be employed for the production of peptides of interest.

BRIEF DESCRIPTION OF THE FIGURES

Figure 1 is a diagram of the plasmid pGBTe418;

Figure 2 is a diagram of the plasmid pGB901;

Figure 3 is a description of the synthesized oligonucleotides for the signal sequence adapted from the amyloglucosidase signal sequence;

Figure 4 is a description of a synthetic signal sequence;

Figure 5 is an immunoblot showing the secretion of prochymosin by K. lactis;

Figure 6 is the sequence of the entire BamHI insert from pDM100PC comprising the fusion peptide of the α-factor of S. cerevisiae and prochymosin and transcriptional regulatory regions;

Figure 7 is a restriction map of plasmid pKS105;

Figure 8 shows the strategy used to design oligonucleotide probes used to identify K. lactis α-factor DNA;

Figure 9 is the complete sequence of a DNA fragment encoding the K. lactis α-factor;

Figure 10 is a description of plasmids employed for expression of the fusion of the α-factor signal sequence and the prochymosin structural gene;

Figure 11 shows the sequences around the junctions in α-factor/prochymosin fusions;

Figure 12 is the sequence of the BamHI/SalI insert of pAB309;

Figure 13 represents the sequences of the primers for mutagenesis of K. lactis α-factor leader DNA;

Figure 14 is a diagram of the plasmid pUCG418;

Figure 15 is a diagram of the plasmid pGBtPA1;

Figure 16 shows the secretion of human t-PA by K. lactis as analysed on a SDS-polyacrylamide gel overlayered with a plasminogen/fibrin-agarose gel;

Figure 17 is a diagram of the plasmid pGBtPA2;

Figure 18 is a diagram of the plasmid pGBHSA3;

Figure 19 shows the secretion of HSA by K. lactis as analysed on a 10% polyacrylamide gel.

DESCRIPTION OF THE SPECIFIC EMBODIMENTS

In accordance with the subject invention, expression cassettes are provided which allow for the efficient and economic production of polypeptides by Kluyveromyces yeast cells. The expression cassettes have transcriptional and translational regulatory sequences functional in a Kluyveromyces host cell and an open reading frame coding for a peptide of interest under the transcriptional and translational control of the regulatory regions. The open reading frame also may include a leader sequence recognized by the Kluyveromyces host which provides for secretion of the polypeptide into the growth medium. The Kluyveromyces cells used may be either laboratory or industrial strains.

The expression cassette will include in the 5'-3' direction of transcription, a transcriptional and translational initiation regulatory region, an open reading frame encoding a peptide of interest, desirably having a signal sequence for secretion recognized by Kluyveromyces, and a translational termination region. The expression cassette will further comprise a transcriptional termination regulatory region. The initiation and termination regulatory regions are functional in Kluyveromyces and provide for efficient expression of the peptide of interest without undesirable effects on the viability and proliferation of the Kluyveromyces host.

The transcriptional and translational initiation regulatory region may be homologous or heterologous to Kluyveromyces. Of particular interest are transcriptional initiation regions from genes which are present in Kluyveromyces or other yeast species, such as Saccharomyces, for example, cerevisiae, Schizosaccharomyces, Candida, etc., or other fungi, for example, filamentous fungi such as Aspergillus, Neurospora, Penicillium, etc. The transcriptional initiation regulatory regions may be obtained for example from genes in the glycolytic pathway, such as alcohol dehydrogenase, glyceraldehyde-3-phosphate dehydrogenase,

(e.g. GM), erythropoietin, thaumatin, insulin, etc.

These structural genes may be obtained in a variety of ways. Where the amino acid sequence is known, the structural gene may be synthesized in whole or in part, particularly where it is desirable to provide yeast-preferred codons. Thus, all or a portion of the open reading frame may be synthesized using codons preferred by Kluyveromyces. Preferred codons may be determined by those codons which are found in the proteins produced in greatest amount by the Kluyveromyces host e.g. glycolytic enzymes. Methods for synthesizing sequences and bringing the sequences together are well established in the literature. Where a portion of the open reading frame is synthesized, and a portion is derived from natural sources, the synthesized portion may serve as a bridge between two naturally occurring portions, or may provide a 3'-terminus or a 5'-terminus. Particularly where the signal sequence and the open reading frame encoding the peptide are derived from different genes, synthetic adaptors commonly will be employed. In other instances, linkers may be employed, where the various fragments may be inserted at different restriction sites or substituted for a sequence in the linker.

For the most part, some or all of the open reading frame will be from a natural source. Methods for identifying sequences of interest have found extensive exemplification in the literature, although in individual situations, different degrees of difficulty may be encountered. Various techniques involve the use of probes, where at least a portion of the naturally occurring amino acid sequence is known, where genomic or cDNA libraries may be searched for complementary sequences. Alternatively, differential transcription can be detected when the gene of interest can be induced or when cells are from the same host but of different differentiation, by comparing the messenger RNA's produced. Other techniques have also been exemplified.

The termination region may be derived from the 3'-region of the gene from which the initiation region was obtained or from a different gene. A large number of termination regions are known and have been found to be satisfactory in a variety of hosts from the same and different genera and species. The termination region is usually selected more as a matter of convenience rather than because of any particular property. Preferably, the termination region will be derived from a yeast gene, particularly Saccharomyces or Kluyveromyces.

In developing the expression cassette, the various fragments comprising the regulatory regions and open reading frame may be subjected to different processing conditions, such as ligation, restriction, resection, in vitro mutagenesis, primer repair, use of linkers and adaptors, and the like. Thus, nucleotide transitions, transversions, insertions, deletions, or the like, may be performed on the DNA which is employed in the regulatory regions and/or open reading frame.

During the construction of the expression cassette, the various fragments of the DNA will usually be cloned in an appropriate cloning vector, which allows for expansion of the DNA, modification of the DNA or manipulation by joining or removing of the sequences, linkers, or the like. Normally, the vectors will be capable of replication in at least a relatively high copy number in E. coli. A number of vectors are readily available for cloning, including such vectors as pBR322, pACYC184, pUC7-19, M13, Charon 4A, and the like.

The cloning vectors are characterized by having an efficient replication system functional in E. coli. Also, the cloning vector will have at least one unique restriction site, usually a plurality of unique restriction sites and may also include multiple restriction sites, particularly two of the same restriction sites for substitution. In addition, the cloning vector will have one or more markers which provide for selection for transformants. The markers will normally provide for resistance to cytotoxic agents such as antibiotics, heavy metals, toxins or the like, complementation of an auxotrophic host, or immunity to a phage. By appropriate restriction of the vector and cassette, and, as appropriate, modification of the ends, by chewing back or filling in overhangs, to provide for blunt ends, by addition of linkers, by tailing, complementary ends can be provided for ligation and joining of the vector to the expression cassette or component thereof.

After each manipulation of the DNA in the development of the cassette, the plasmid will be cloned and isolated and, as required, the particular cassette component analyzed as to its sequence to ensure that the proper sequence has been obtained. Depending upon the nature of the manipul ation, the desired sequence may be excised from the plasmid and introduced into a different vector or the plasmid may be restricted and the expression cassette component manipulated, as appropriate.

In some instances a shuttle vector will be employed where the vector is capable of replication in different hosts requiring different replication systems. This may or may not require additional markers which are functional in the two hosts. Where such markers are required, these can be included in the vector, where the plasmid containing the cassette, the two replication systems, and the marker(s) may be transferred from one host to another, as required. In the present situation, the second replication system would be a replication system functional in Kluyveromyces. The replication systems which may be used

dihydrofolate reductase, metallothioneins, thymidine kinase, etc., have proven useful in a variety of hosts to provide for amplification, where the gene provides protection from a toxin, such as methotrexate, heavy metals, such as copper and mercury, and the like.

Vectors of interest providing for stable replication include KARS vectors originating from K. lactis, e.g. pKARS12 and pKARS2, which plasmids comprise a K. lactis DNA fragment containing the KARS12 or KARS2 sequence in the S. cerevisiae plasmid YRp7. A vector employed for integration is, for example, pL4, a hybrid plasmid of the ARS1 carrying plasmid YRp7 and K. lactis XhoI DNA fragment carrying the LAC4 gene. See EP-A 0096430.

Plasmids of particular interest include plasmids having the 2 micron plasmid replication system, the LAC4 gene, the Tn601 and Tn5 kanamycin resistance gene, which also provides resistance to the antibiotic G418 in Kluyveromyces (Jimenez and Davis, Nature (1980) 287:869-871). This plasmid provides for autonomous replication in Kluyveromyces and can be selected for by resistance to G418 on regeneration plates containing glucose, sorbitol, and 0.2 µg/ml G418, while avoiding elevated concentrations of KC1, which interferes with the sensitivity of Kluyveromyces to G418. Preferred plasmids include the TRP1 gene, particularly from S. cerevisiae, the LAC4 gene, particularly from K. lactis the Kan^R gene providing for resistance against antibiotic G418 from Tn5, or the like.

The subject vectors and constructs are introduced into an appropriate host for cloning and expression of the desired structural genes. After transformation, colonies will normally appear on regeneration medium within about 5 to 6 days. Where an antibiotic is employed for selection, the colonies should be screened to ensure the absence of spontaneous mutation to a resistant strain. Employing the plasmids and the methods of the subject invention, about 5% of resistant colonies were found to contain the plasmid construct providing for at least about 4 transformants per µg of plasmid DNA. Where selection was based on the presence of the LAC4 gene, using plates containing lactose as the sole carbon source and 0.6M KCl as an osmotic stabilizer, all of the surviving colonies were found to be transformants and not spontaneous revertants. About 20 transformants were obtained after about 4 to 5 days of incubation at moderate temperature, e.g. 30° C.

As a host organism, Kluyveromyces is especially suitable for the production of heterologous proteins, for example for the production and extraction of the enzyme chymosin and its precursors preprochymosin, pseudochymosin and prochymosin, for human serum albumin (HSA), tissue plasminogen activator (t-PA), and thaumatin and its precursor forms. Although other organisms such as Saccharomyces produce prochymosin in reasonable amounts, the produced prochymosin cannot be extracted in an active or activatable form. We have surprisingly found that more than 90% of the total amount of the prochymosin produced by Kluyveromyces can be extracted in an active form with very simple standard techniques.

Any of the many Kluyveromyces species may be employed. Either laboratory or industrial, preferably industrial, strains may be used. By industrial species is intended, Kluyveromyces strains from organisms which may be isolated from natural sources or may be available from depositories or other sources or obtained by modification, e.g. mutation, of such strains. The industrial strains are characterized by being resistant to genetic exchange, being prototrophic or made prototrophic by a single gene being introduced into the host strain, and are usually selected for improved production of peptides. Among the Kluyveromyces species which may find use are K. lactis, K. fragilis, K. bulgaricus, K. thermotolerans, K. marxianus, etc. It should be further noted that the Kluyveromyces organisms are on the GRAS (Generally Recognized As Safe) list. Their use for production of products to be used in vivo or to be ingested normally will not require special governmental review and approval.

Both wild type and mutant Kluyveromyces, particularly Kluyveromyces lactis or Kluyveromyces fragilis may be employed as hosts. Hosts of particular interest include K. lactis SD11 lac4 trp1 and K. lactis SD69 lac4, and the wild-type strain CBS 2360 (see EP-A-0096430).

For maintaining selective pressure on the transformants for maintenance of the plasmids, selective media may be used, such as a yeast nitrogen-based medium, 2% lactose instead of glucose for K. lactis SD69 lac4 (PTY75-LAC4) and for K. lactis SD69 lac4 (pL4) and a yeast nitrogen-based medium (Difco) plus 2% glucose for K. lactis SD11 lac4 trp1 (pKARS12). See for the transformants mentioned, EP-A-0096430. Similarly, strains containing plasmids conferring antibiotic resistance, for example against G418, may be cultivated in a medium containing said antibiotic.

Where the hybrid plasmids are employed for large scale production of the desired protein, it would generally be useful to remove at least substantially all of the bacterial DNA sequences from the hybrid plasmids.

Depending upon the nature of the structural gene of interest, the expression product may remain in the cytoplasm of the host cell or be secreted. It has been found that not only the proteins that remain in the cell but also those that are secreted are soluble. Where the expression product is to remain in the host cell, it

C. Construction of plasmid pGB900 containing the G418 resistance gene and prochymosin encoding DNA

The 3.6 kb HindIII-XbaI fragment from plasmid pGBTeG418 containing the G418 resistance gene (see Example 1B) and the SalI-HindIII fragment containing the prochymosin gene from pGB123 (see EP-A-0096430) were ligated in pUC19 cleaved with SalI and XbaI. This yielded plasmid **pGB900**.

D. Construction of plasmid pGB901 (see Figure 2)

Plasmid **pGB901** was constructed by ligating the following four fragments:

(1) a 3.6 kb XbaI-HaeII fragment containing the lactase promoter to about position -90 from the lactase ATG start codon isolated from pUCla56,

(2) a HaeII-SalI fragment extending from the above HaeII site to a SalI site, which was ligated to position -26 in a similar Bal31 experiment as described in Example 16.C2 of EP-A-0096430. However, in this experiment only a SalI linker was used. This fragment has the following sequence.

(3) the 5.1 kb SalI-XbaI fragment containing prochymosin and G418 from pGB900 (see Example 1C),

(4) pUC19 cleaved with XbaI.

During the construction of the plasmid the CG sequence from the HaeII site was inadvertently removed, thereby creating a HindIII site at this position.

Prochymosin-encoding DNA is present in plasmid pGB901. This may readily be converted to plasmids with preprochymosin, pseudochymosin or chymosin DNA by using the SalI-BglII fragments from pGB 131, 122 or 124, respectively (see Ep-A-0096430).

Example 2

Secretion of prochymosin from Kluyveromyces lactis transformants

To direct the synthesis of prochymosin in Kluyveromyces, plasmid pGB901 was used to transform K. lactis strains SD11 and CBS 2360 with similar results. The transformation was carried out essentially as described in Examples 4 and 14 of EP-A-0096430, by using intact plasmid DNA or plasmid DNA cut with restriction endonucleases. In the latter case restriction endonucleases were used which cut in the promoter region, e.g., SacII, NdeI, SnaBI or SpeI, or in the terminator region, e.g., EcoRV, or both the promoter and terminator regions.

K. lactis strain CBS 2360 was grown in 100 ml of YEPD-medium (1% yeast extract, 2% peptone, 2% glucose) containing 2.5 ml of a 6.7% yeast nitrogen base (Difco) solution to an OD_{610} of about 7. The cells were collected by centrifugation from 10 ml of the culture, washed with TE-buffer (10 mM Tris-HCl pH 7.5, 0.1 mM EDTA) and resuspended in 1 ml TE-buffer. An equal volume of 0.2 M lithium acetate was added and the mixture was incubated for 1 hr at 30° C in a shaking waterbath. Plasmid pGB901 (15 µg) was cut at the unique SacII site in the lactase promoter, ethanol precipitated and resuspended in 15 µl TE-buffer. This DNA preparation was added to 100 µl of the pre-incubated cells and the incubation was prolonged for 30 minutes. Then an equal volume of 70% PEG 4000 was added and the mixture was incubated for 1 hr at the same temperature, followed by a heatshock of 5 minutes at 42° C. Then 1 ml of YEPD-medium was added and the cells were incubated for 1.5 hrs in a shaking waterbath of 30° C. Finally the cells were collected by centrifugation, resuspended in 300 µl YEPD and spread on agar plates containing 15 ml of YEPD agar with 300 µg/ml of G418, overlayered (1 hr before use) with 15 ml YEPD-agar without G418. Colonies were grown for 3 days at 30° C. K. lactis strain SD11 was transformed in a similar way, only the initial G418 concentration in the selection plates was lowered to 150 µg/ml. In one of the experiments transformants of

Protein synthesis starts at the boxed ATG codon.

Example 4

Expression of preprochymosin by Kluyveromyces transformants

The SalI site from the polylinker of pGB902 (see Example 3) was removed for convenience. pGB902 was partially digested with SalI, followed by a short incubation with Bal31 (Boehringer). Linear fragments were isolated from an agarose gel, ligated and transformed into E. coli. A correct plasmid, **pGB903**, was obtained. Restriction analysis showed that this plasmid also has the XbaI and HindIII sites removed from the polylinker.

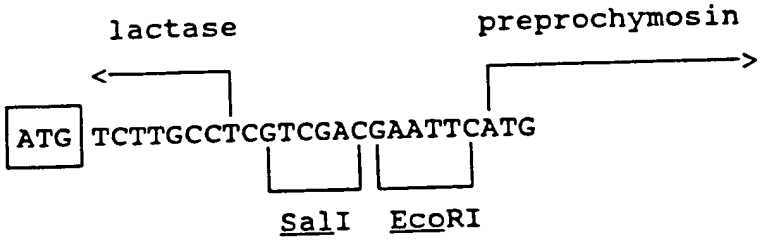
To construct a plasmid containing and expressing preprochymosin, plasmid pGB903 was digested with the restriction endonucleases SalI and BglII. The 11 kb DNA fragment was isolated from an agarose gel by electroelution. Similarly, plasmid pGB124 containing the preprochymosin gene (see EP-A-0096430, Example 16) was digested and the 0.3 kb SalIBglII fragment containing the N-terminal part of the preprochymosin gene was isolated.

The 11 kb and the 0.3 kb DNA fragments were mixed, ligated with DNA ligase and transformed into E. coli. Plasmid **pGB904** was isolated which contained the preprochymosin gene fused to a small part of the lactase gene (Table 2).

Table 2

Nucleotide sequence at the junction between the lactase promoter and preprochymosin in pGB904

pGB904



Protein synthesis starts at the boxed ATG codon.

K. lactis CBS 2360 cells were transformed with pGB904, which had been linearized with SacII. Transformants were selected, grown and assayed for chymosin activity as described in Example 2. In the following Table 3 a comparison is made between the secretion of prochymosin from K. lactis CBS 2360 cells transformed with pGB902 (see Example 3) and with pGB904. (Pro)chymosin production is expressed in arbitrary units per ml of cells at OD_{610} of 200.

Table 4

Secretion of prochymosin by K. lactis cells transformed with pGB902 and pGB905				
Transformant	pGB902		pGB905	
	Supernatant	Pellet	Supernatant	Pellet
1.	3.2	<0.4	60.6	<0.4
2.	1.3	<0.4	56.4	<0.4
3.	7.1	1.4	56.7	<0.4
4.	4.4	0.66	57.6	<0.4

B. Chemical synthesis of a novel synthetic leader sequence into construction of a plasmid containing the novel synthetic leader sequence.

A synthetic leader sequence was prepared which has a sequence different from any known leader sequence. Using this leader sequence, all prochymosin synthesized was secreted by Kluyveromyces as shown below.

This synthetic leader sequence was devised using frequently occurring amino acids from position -6 to +2 of the signal sequence cleavage site (Von Heyne, Eur. J. Biochem. (1983) 133:17-21). Frequently occurring yeast codons were also employed and extra nucleotides were incorporated in front of the ATG sequence to make up for the deletion of 26 nucleotides in pGB902. The oligonucleotides used and the resulting leader sequence are shown in Figure 5.

The synthetic leader sequence DNA was synthesized using an Applied Biosystems DNA synthesizer. The resulting oligonucleotides were run on a 40 cm long, 1 mm thick polyacrylamide gel, containing TBE buffer (50 mM Tris, 50 mM borate, 1mM EDTA, pH 8.3) and 7 M urea until the Bromophenol Blue marker had travelled 2/3 of the gel length. The DNA was visualized, eluted from the gel and precipitated with ethanol.

Also from pGB901 a derivative was made with a deletion around the SalI site resulting from the polylinker of pUC19. This was done by replacing the 0.5 kb SnaBI-BglII fragment from pGB903 by the corresponding fragment from pGB901. The resulting plasmid was cut at the unique SalI site. The oligonucleotides were hybridized at 65°C, 50°C and 37°C for one hour each in 2xSSC. The DNA was ligated into the SalI site using T4 polynucleotide ligase. The plasmid was then transformed into E. coli HB101. Of the colonies obtained, 24 were cultured and plasmid DNA isolated. One of the plasmids, **pGB906**, was shown to have the oligonucleotides in the correct orientation by restriction enzyme digestion. It was found that K. lactis CBS 2360 transformed with pGB906 secreted more than 95% of the prochymosin produced.

C. Analysis of chymosin protein produced by K. lactis transformed with pGB905

K. lactis CBS 2360 (pGB905) transformants were grown for 3 days at 30°C and samples were collected from the supernatant of the cultures. Protein samples were electrophoresed on a polyacrylamide gel according to Laemmli (Nature (1970) 227:680-685). Proteins were blotted onto a nitrocellulose filter according to the method of Towbin et al. (Proc. Natl. Acad. Sci. USA (1979) 76:4350-4354). Chymosin protein was detected by incubating the filter with a polyclonal antiserum against chymosin (Chr. Hansen), followed by donkey anti-rabbit antibodies coupled to a peroxidase (Amersham) and finally with 0.6 mg/ml 4-chloronaphthol and 0.015% hydrogen peroxide in a buffer solution (50 mM Tris-HCl pH 7.5, 0.9% NaCl) containing 40% methanol. Prochymosin excreted by the AG signal sequence is correctly cleaved after pH 2 treatment as demonstrated by this assay (Figure 5). Similar results were obtained with K. lactis CBS 2360 (pGB906) transformants.

Table 5

Prochymosin production in K. lactis and S. cerevisiae transformants		
Strain	Chymosin Activity (relative units/ml culture)	
	Cell Extract	Culture Supernatant
AB110	<0.25	<1.0
AB110::pKS100	15.5	2.3
KRN201-6	<0.25	<1.0
KRN201-6::pKS100	12.0	333.0

Plasmid pAB300 was used to transform K. lactis strain 2UV21 to G418 resistance, targeting integration to the EcoRV site in the 3′ region of the LAC4 gene. These transformants were also found to efficiently secrete prochymosin into the culture medium as shown in Table 6 below.

Table 6

Prochymosin secretion from α-factor:prochymosin fusions		
Host Strain	Transforming Plasmid	Secreted Chymosin Activity (relative units/ml culture)
2UV21	-	<2
KRN201-6	-	<2
KRN201-6	pKS100	385
2UV21	pAB300	294

B. Construction of LAC4 promoter/α-factor leader/prochymosin fusions

In order to produce this fusion, two intermediate plasmids were constructed. Plasmid pDM100-PC was partially digested with PstI, ligated to a SalI-PstI adaptor encoding a portion of the α-factor leader and 26 bp of the region 5′ to the LAC4 gene, and then digested with HindIII. A 1500 bp fragment was isolated from this mixture and then cloned into pUC18 digested with HindIII and SalI to produce **pKS102**.

A synthetic E. coli lac operator was ligated into the SalI site just 5′ to the α-factor leader coding sequence in pKS102 to produce the plasmid **pKS103**. This was done because the LAC4 promoter/α-factor leader/prochymosin fusion may be toxic to E. coli.

A 490 bp SalI-BglII fragment from pKS103 was isolated and ligated to SalI-BglII-digested pJD15R. Plasmid pJD15R is derived from pGB901 by deletion of the SalI site in the pUC19 polylinker by filling-in to produce pJD15, and then recloning the 8800 bp XbaI fragment in the opposite orientation. From this reaction the plasmid **pKS105** was isolated. These plasmids are illustrated in Figure 7.

Plasmid pKS105 was then used to transform K. lactis strain CBS 2360 to G418 resistance, using the SacII site in the LAC4 5′ region as a targeting site for the integrative transformation. Chymosin production is expressed in units per ml of cells at OD_{610} of 200, see Table 7 below.

enzymes and the resulting fragments analyzed by Southern blot analysis using the same hybridization probes in order to identify restriction fragments of size suitable for DNA sequence analysis. Fragments thus identified were purified by agarose gel electrophoresis and cloned into appropriate MP18 and MP19 vectors. DNA sequence analysis was then performed.

C. Isolation of Kluyveromyces α-factor

The first 10 amino acids of the K. lactis α-factor showed a definite homology to that from S. cerevisiae, with 6 identical residues. This sequence is shown below:

Trp-Ser-Trp-Ile-Thr-Leu-Arg-Pro-Gly-Gln

This protein sequence was used to design a set of oligonucleotides deduced to be complementary to the structural gene for the corresponding structural gene as shown in Figure 8. Oligonucleotides including all of the possible codons for a segment of the α-factor peptide were synthesized as two pools of 96 and 48 different molecules.

These two pools were radioactively labeled using γ-[^{32}P]-ATP and T4 polynucleotide kinase, and were each used to probe a Southern blot of restriction digests of K. lactis DNA. Pool #2 gave strong hybridization to a single fragment and much weaker hybridization to a second fragment in several different digests. Thus, pool 2 was chosen to screen plasmid libraries of K. lactis genomic DNA.

Use of these probes to screen plasmid libraries resulted in the isolation of a number of hybridizing clones. DNA sequence analysis of one of these clones, αfk18b, showed it encodes an α-factor related peptide which bears a strong similarity to the precursor of the S. cerevisiae α-factor peptide. The hybridizing segment was located on a PstI-EcoRI fragment of about 1000 bp. The sequence of this fragment is shown in Figure 9. The K. lactis precursor contains only 2 sites for the addition of N-linked carbohydrate chains. In addition, the spacers of the K. lactis repeats are longer than those of the S. cerevisiae repeats and show a more diverse sequence with the pattern X-Ala/Pro rather than the Glu/Ala-Pro sequences found in S. cerevisiae. A comparison of the DNA sequences showed a strong degree of homology throughout the coding region.

D. Construction of Plasmids

A series of plasmids (shown in Figure 10) were constructed in order to provide a fusion of the K. lactis α-factor leader to prochymosin expressed under the transcriptional control of a strong promoter.

pAB307: A 673 bp SspI-EcoRI fragment from αfk18b (Figure 9) was modified by filling the EcoRI overhang by Klenow enzyme and addition of BglII linkers to the blunt ends. This fragment was then inserted into a BglII site joining the promoter and terminator regions of the S. cerevisiae glyceraldehyde-3-phosphate dehydrogenase gene (GAPDH). This cassette was cloned as a BamHI fragment in pUC18, resulting in pAB307.

pAB309: Fusion of sequences encoding the α-leader and bovine prochymosin was then performed. First pAB307 was digested with NcoI and the cohesive ends made blunt by treatment with mung bean nuclease. The resulting product was then digested with SalI. To this was ligated a 2000 bp EcoRV-SalI fragment containing sequences encoding prochymosin and the S. cerevisiae transcriptional termination region. This fragment was derived from plasmid pJS111 in which a XbaI-BamHI adaptor had been added to the 5′ end of a fragment containing prochymosin cDNA fused to the S. cerevisiae GAPDH transcriptional termination region. This ligation mixture was used to transform E. coli strain HB101 and a transformant carrying the plasmid pAB309 was isolated. The sequences around the junction of this fusion are shown in Figure 11 and the sequence of the entire BamHI-SalI insert of pAB309 is shown in Figure 12.

pAB312: In order to obtain transformation of K. lactis strains, a 3560 bp HindIII fragment derived from pGB901 was inserted into pAB309 producing plasmid pAB312. The HindIII fragment contains the 3′ region of the K. lactis LAC4 gene and a fusion of the S. cerevisiae ADH1 promoter to the bacterial G418-resistance structural gene.

pAB313 and **pAB314**: A 1900 bp SacI-HindIII was isolated from pAB309 and cloned into MP19 (Yanisch-Perron et at., Gene (1985) 33:103). Single-stranded phage DNA was prepared and used as a template for in vitro mutagenesis with one of the two oligonucleotide primers shown in Figure 13. The M13

Example 8

Secretion of t-PA by Kluyveromyces lactis using an amyloglucosidase signal sequence

A. Cloning of tissue-type plasminogen activator cDNA

A cDNA coding for tissue-type plasminogen activator (t-PA) was obtained in a way similar to that described by Pennica et al. (Nature (1983) 301:214). DNA sequence analysis and restriction mapping confirmed the authenicity of the t-PA cDNA. For expression studies the 2.0 kb BglII fragment (see Pennica et al.), comprising almost the complete coding region for the mature protein and the 3′ noncoding region, was used.

B. Introduction of the G418 resistance marker in pUC19

A DNA fragment comprising the Tn5 gene (Reiss et al., EMBO J. (1984) 3:3317), conferring resistance to G418 under the direction of the alcohol dehydrogenase I (ADHI) promoter from S. cerevisiae similar to that described by Bennetzen and Hall, J. Biol. Chem. (1982) 257:3018, was inserted into the SmaI site of pUC19 (Yanisch-Perron et al., Gene (1985) 33:103). The obtained plasmid, **pUCG418**, is shown in Figure 14. E. coli containing pUCG418 was deposited at Centraal Bureau voor Schimmelcultures on December 4, 1987 under CBS 872.87.

C. Construction of pGBtPA1

In a few cloning steps **pGBtPA1** was constructed (see also Figure 15 and Table 9) containing the following elements:

(1) pUCG418 (see above) cut with XbaI and HindIII;

(2) the XbaI-SalI fragment from pGB901, containing the lactase promoter;

(3) synthetic DNA coding for the signal sequence of amyloglucosidase from Aspergillus awamori - (Innis et al., Science (1985) 228:21). The sequence in front of the startcodon was chosen to remove the SalI site at the end of the lactase promoter fragment and further comprises part of the 5′ noncoding region of the lactase gene;

(4) the 2.0 kb BglII fragment from the t-PA cDNA (see above);

(5) synthetic DNA, comprising part of the 3′ noncoding region of the lactase gene.

Table 10

Clotlysis assay of the cultures from CBS 2360 and from CBS 2360 transformed with pGBtPA1	
transformant	t-PA activity in supernatant
1	40 µg/l
2	6 µg/l
3	<3 µg/l
4	<3 µg/l
5	25 µg/l
6	3 µg/l
7	3 µg/l
8	<3 µg/l
9	3 µg/l
10	<3 µg/l
CBS 2360 1°)	<3 µg/l
CBS 2360 2°)	<3 µg/l
CBS 2360 3°)	<3 µg/l
CBS 2360 4°)	<3 µg/l
CBS 2360 5°)	<3 µg/l

In some of the cell extracts a slight t-PA activity (≤ 3 µg/l) was found.

Analysis was also performed on SDS-polyacrylamide gels overlayered with a plasminogen/fibrin-agarose gel according to Granelli-Piperno and Reich (J. Exp. Med. (1978) 148:223). 200 µl of the supernatant of a culture of CBS 2360 or CBS 2360 transformed with pGBtPA1 was precipitated with ethanol and resuspended in 20 µl sample buffer (62.5 mM Tris-HCl pH 6.8, 2% sodium dodecylsulphate, 10% glycerol, Bromophenol Blue). The samples were layered on the gels without prior boiling. The results (shown in Figure 16) demonstrate the secretion of human t-PA by K. lactis. Furthermore, it is clear that most of the secreted material is glycosylated.

The secretion of t-PA was also confirmed by using an ELISA with a monoclonal antibody against human t-PA (ESP5 purchased from Biopool) and by a chromogenic activity assay (a commercial test from Kabi Vitrum).

Example 9

Secretion of t-PA by Kluyveromyces lactis using the signal seqence from human serum albumin

A. Construction of pGBtPA2

In a few cloning steps **pGBtPA2** was constructed (see Figure 17 and Table 11), containing the following elements :

(1) pUCG418, cut with XbaI and HindIII;
(2) the XbaI-SalI fragment from pGB901, containing the lactase promoter;
(3) synthetic DNA coding for the prepro-region of human serum albumin;
(4) the 2.0 kb BglII fragment from the t-PA cDNA (see Example 8);

(3) synthetic DNA (SalI-HindIII fragment), comprising part of the 3' noncoding region of the lactase gene. The sequence of this fragment is given in Table 13.

Table 13

Sequence of the SalI - HindIII fragment of pGBHSA1

```
                              EcoRV
SalI   NotI      BglII        XhoI
 v      v          v     v     v
 TCGACGCGGCCGCAGATCTGATATCTCGAGAATTTATACTTAGATAAGTATGTACTTACA
     GCGCCGGCGTCTAGACTATAGAGCTCTTAAATATGAATCTATTCATACATGAATGT

                                                    HindIII
                                                      v
GGTATATTTCTATGAGATACTGATGTATACATGCATGATAATATTTAA
CCATATAAAGATACTCTATGACTACATATGTACGTACTATTATAAATTTCGA
```

C. Construction of pGBHSA2

pGBHSA1 was cut with SalI and EcoRV and synthetic DNA was inserted:

```
SalI                  BstEII          StuI
 v                      v              v
  TCGACAAAAATGAAGTGGGTAACCATCGATAGGCCTACTGGGCTCGAGATC
      GTTTTTACTTCACCCATTGGTAGCTATCCGGATGACCCGAGCTCTAG
```

The underlined ATG-codon indicate the initiation codon in the ultimate expression construct (pGBHSA3, see below).

The resulting plasmid was named **pGBHSA2**.

D. Construction of pGBHSA3

The HSA cDNA-clone was cut with HindIII and the sticky end was filled in, using Klenow DNA polymerase I. Subsequently the DNA was cut with BstEII and the BstEII-HindIII (filled in) fragment, containing almost the complete HSA coding region was purified. pGBHSA2 was digested with XhoI, the sticky ends were filled in using Klenow DNA polymerase I and digestion with BstEII was performed. In the resulting vector the HSA encoding fragment (BstEII-HindIII (filled in)) was inserted. The obtained plasmid, **pGBHSA3**, is shown in Figure 18.

E. Transformation of Kluyveromyces lactis and analysis of the transformants

Transformation of K. lactis strain 2360 with PGBHSA3 was performed as described in Example 2. Transformants and the control strain CBS 2360 were grown in YEPD medium for about 64 hrs at 30° C. The cells were separated from the culture medium by centrifugation. Samples of 30 µl were taken from the supernatants and analysed by electrophoresis on a 10% polyacrylamide gel according to Laemmli (Nature 227, 680 (1970)). The results shown in Figure 19 demonstrate that HSA is secreted into the culture medium by K. lactis cells transformed with pGBHSA3. There is also an indication that the secretion of other proteins is reduced in the HSA producing cells.

The above results demonstrate that one can obtain efficient, convenient expression of exogenous genes in Kluyveromyces strains. Furthermore, the Kluyveromyces strains appear to be particularly useful for providing highly efficient secretion and processing of a wide variety of proteins, as illustrated by the results with prochymosin. Constructs and vectors are provided which allow for the introduction of an exogenous gene under the regulatory control of efficient promoters in Kluyveromyces and, as desired, joining to signal sequences which provide for translocation of the exogenous gene, particularly secretion. Thus, a fermentation system is provided for commercial production of a wide variety of exogenous proteins in an active or activatable form.

The following organisms have been deposited with the American Type Culture Collection on June 30, 1987: 2UV21, ATCC Accession No. 20855; KRN201-6, ATCC Accession No. 20854; HB101 pAB307, ATCC Accession No. 67454; HB101 pAB312, ATCC Accession No. 67455.

Although the foregoing invention has been described in some detail by way of illustration and example for purposes of clarity of understanding, it will be obvious that certain changes and modifications may be practiced within the scope of the appended claims.

Claims

1. A method for producing a polypeptide of interest in a Kluyveromyces host cell, said method comprising:
introducing into said host cell a DNA sequence encoding said polypeptide of interest and
growing said host cell comprising said DNA sequence in a culture medium whereby said polypeptide of interest, or part thereof, is secreted into the culture medium.

2. A method according to Claim 1, whereby said DNA sequence forms part of a DNA construct which is introduced into said host cell and which comprises, in the direction of transcription, a transcriptional initiation regulatory region functional in said host cell; said DNA sequence encoding said polypeptide of interest; and a transcriptional termination regulatory region functional in said host cell.

3. A method according to Claim 1 or 2, wherein a signal sequence heterologous to said host cell or to said polypeptide of interest, or to said host and to said polypeptide of interest is joined in reading frame to the 5' terminus of said DNA sequence, whereby said polypeptide of interest is secreted by said host cell.

4. A method according any one of Claims 1 to 3, wherein said polypeptide of interest is an enzyme.

5. A method according to Claim 4, wherein said enzyme is chymosin, or a precursor thereof.

6. A method according to Claim 4, wherein said enzyme is tissue plasminogen activator (t-PA), or mutant forms thereof.

7. A method according to any one of the Claims 1 to 3, wherein said polypeptide of interest is human serum albumin (HSA).

8. A method according to any one of Claims I to 7, wherein said host cell is an industrial strain of Kluyveromyces.

9. A method according to any one of Claims to 8, wherein said host cell is K. lactis or K. fragilis.

10. A method according to Claim 2, wherein said DNA construct further comprises at least one of a selection marker, a replication system for autonomous replication of said DNA sequence, or a transformation efficiency enhancing sequence.

11. A method according to Claim 10, wherein said replication system is an autonomously replicating sequence (ARS).

12. A method according to Claim 11, wherein said autonomously replicating sequence is a Kluyveromyces autonomously replicating sequence (KARS).

13. A method according to Claim 10, wherein said selection marker is resistance to G418.

14. Use of Kluyveromyces as a host for the transformation and expression of foreign genes and the secretion of the polypeptide encoded by said gene, or secretion of part of said polypeptide.

15. A transformed Kluyveromyces host cell comprising an expression cassette which comprises, in the direction of transcription, a transcriptional initiation regulatory region functional in said host cell, a signal sequence functional in said host cell joined in reading frame with a DNA sequence encoding a polypeptide of interest, and a transcriptional termination regulatory region functional in said host cell.

16. A cell according to Claim 15, wherein said signal sequence is heterologous to said host cell or to said poly peptide of interest or to said host cell and to said polypeptide of interest.

17. A cell according to Claim 16, wherein said signal sequence is the α-factor signal sequence form Saccharomyces cerevisiae.

European Patent Office

EUROPEAN SEARCH REPORT

Application number

EP 88201632.2

DOCUMENTS CONSIDERED TO BE RELEVANT

Category	Citation of document with indication, where appropriate, of relevant passages	Relevant to claim	CLASSIFICATION OF THE APPLICATION (Int Cl 4)
D,X	EP - A1 - 0 096 430 (GIST-BROCADES N.V.) * Claims 1-5,8-10,12,23,24,27, 37 * --	1-5, 8-12, 14-16	C 12 N 15/00 C 12 P 21/00 C 12 N 1/16 C 12 N 5/00 C 07 H 21/04
X	EP - A1 - 0 096 910 (UNILEVER NV) * Claims 1,2 * --	1-3, 8,9, 14,15	
P,X	EP - A2 - 0 241 435 (UNIVERSITA DEGLI STUDI DI ROMA) * Claims 7-9 * --	1,8, 9,14	
A	EP - A1 - 0 116 201 (CHIRON CORPORATION) * Claims 1-5 * ----	15,17	

TECHNICAL FIELDS SEARCHED (Int. Cl.4)

C 12 N
C 12 P
C 07 H

The present search report has been drawn up for all claims

Place of search	Date of completion of the search	Examiner
VIENNA	07-11-1988	WOLF

CATEGORY OF CITED DOCUMENTS

X : particularly relevant if taken alone
Y : particularly relevant if combined with another document of the same category
A : technological background
O : non-written disclosure
P : intermediate document

T : theory or principle underlying the invention
E : earlier patent document, but published on, or after the filing date
D : document cited in the application
L : document cited for other reasons

& : member of the same patent family, corresponding document

EPO Form 1503 03.82